

**EXHIBIT B:**

**MULTISPECIES COMPARISON OF STRAD POLYPEPTIDE**

**BLAST****Basic Local Alignment Search Tool**

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

**STRAD comparison**

Results for:

ref|NP\_001003787.1 STE20-related kinase adapter protein alpha isoform 1 [Homo sapiens] >gi|74759034|sp|Q7RTN6.1|STRAA\_... (431aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

gi|51242955|ref|NP\_001003787.1|

gi|51242955|ref|NP\_001003787.1|

**Description**

STE20-related kinase adapter protein alpha isoform 1 [Homo sapiens] >gi|74759034|sp|Q7RTN6.1|STRAA\_HUMAN RecName:

Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein; AltName: Full=Serologically defined breast cancer antigen NY-BR-96 >gi|34494889|tpg|DAA01797.1| TPA\_exp: STE20-related adaptor protein [Homo sapiens] >gi|119614691|gb|EAW94285.1| protein kinase LYK5, isoform CRA\_c [Homo sapiens]

**Molecule type**

amino acid

**Query Length**

431

**Subject ID**

4 subjects

**Description****Molecule type**

amino acid

**Subject Length**

n/a

**Program**

BLASTP 2.2.24+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

[Reference - compositional score matrix adjustment](#)

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)

[Search Parameters](#)

**Search parameter name Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hillist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

**Params Ungapped Gapped**

Lambda	0.318619	0.267
K	0.13404	0.041
H	0.398234	0.14

Results Statistics

**Results Statistics parameter name Results Statistics parameter value**

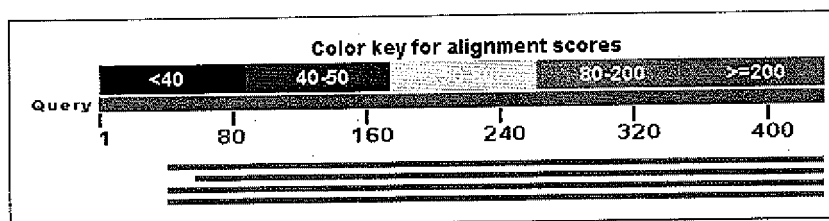
Effective search space	144800
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## Graphic Summary

### Distribution of 4 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



## Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay  
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
<a href="#">XP_850260.1</a>	PREDICTED: similar to protein kinase LYK5 isoform 2 isoform 1 [Canis familiaris]	786	786	90%	0.0	<a href="#">UGM</a>
<a href="#">NP_001015603.1</a>	STE20-related kinase adapter protein alpha [Bos taurus] >gi 240849233 ref NP_001155356.1  STE20-related kinase adapter protein alpha [Ovis aries] >gi 75070042 sp Q5E9J9.1 STRAA_BOVIN RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gi 59858207 gb AA08938.1  protein kinase LYK5 isoform 4 [Bos taurus] >gi 238566930 gb ACR46653.1  STRADA [Ovis aries]	748	748	86%	0.0	<a href="#">UGM</a>
<a href="#">NP_082402.1</a>	>gi 296476245 gb DAA18360.1  STE20-related kinase adapter protein alpha [Bos taurus] >ref NP_001155356.1  STE20-related kinase adapter protein alpha [Ovis aries] >sp Q5E9J9.1 STRAA_BOVIN RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gb AA08938.1  protein kinase LYK5 isoform 4 [Bos taurus] >gb ACR46653.1  STRADA [Ovis aries] >gb DAA18360.1  STE20-related kinase adapter protein alpha [Bos taurus]  STE20-related kinase adapter protein alpha [Mus musculus] >gi 12847582 db BAB27626.1  unnamed protein product [Mus musculus] >gi 33638094 gb AAQ24157.1  protein kinase LYK5 splice variant 1 [Mus musculus] >gi 35192984 gb AAH58517.1  RIKEN cDNA 2610019A05 gene [Mus musculus] >gi 117616946 gb ABK42491.1  STLK5 [synthetic construct] >gi 123243203 emb CAM27017.1  novel protein [Mus musculus] >gi 148702325 gb EDL34272.1  RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus] >gi 148702326 gb EDL34273.1  RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus] >db BAB27626.1  unnamed protein product [Mus musculus] >gb AAQ24157.1  protein kinase LYK5 splice variant 1 [Mus musculus] >gb AAH58517.1  RIKEN cDNA 2610019A05 gene [Mus musculus] >gb ABK42491.1  STLK5 [synthetic construct] >emb CAM27017.1  novel protein [Mus musculus] >gb EDL34272.1  RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus] >gb EDL34273.1  RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus]  STE20-related kinase adapter protein alpha [Rattus norvegicus] >gi 81912054 sp Q7TNZ6.1 STRAA_RAT RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gi 33087213 gb AAP92801.1  protein kinase LYK5 [Rattus norvegicus] >sp Q7TNZ6.1 STRAA_RAT RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gb AAP92801.1  protein kinase LYK5 [Rattus norvegicus]	775	775	90%	0.0	<a href="#">UGM</a>
<a href="#">NP_877972.1</a>	>gi 81912054 sp Q7TNZ6.1 STRAA_RAT RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gi 33087213 gb AAP92801.1  protein kinase LYK5 [Rattus norvegicus] >sp Q7TNZ6.1 STRAA_RAT RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gb AAP92801.1  protein kinase LYK5 [Rattus norvegicus]	758	758	90%	0.0	<a href="#">UGM</a>

## Alignments

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)

>ref|XP\_850260.1| [UGM](#) PREDICTED: similar to protein kinase LYK5 isoform 2 isoform 1 [Canis familiaris]  
Length=394

GENE ID: 609377 STRADA | STE20-related kinase adaptor alpha  
[Canis lupus familiaris]

Score = 786 bits (2030), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 376/390 (97%), Positives = 381/390 (98%), Gaps = 0/390 (0%)

```

Query 42  TNDASSESIASFQKQEVMSFLPEGGCYELLTIVIGKGFEDIMTVNLARYKPTGEYVTVRR 101
          TN+ASSESIAS SKQE+MSSFLPEGG YELLT+IGKGFEDIMTVNLARYKPTGEYVTVRR
Sbjct 5    TNEASSESTASLSKQEIIMSSFLPEGGRYELLTIIIGKGFEDIMTVNLARYKPTGEYVTVRR 64

Query 102 INLEACSNEMVTFQLGELHVSCLFHPNIPYRATFIADNELWVVTSMAYGSAKDLICT 161
          INLEACSNEMVTFQLGELHVSCLFHPNIPYRATFIADNELWVVTSMAYGSAKDLICT
Sbjct 65  INLEACSNEMVTFQLGELHVSCLFHPNIPYRATFIADNELWVVTSMAYGSAKDLICT 124

Query 162 HFMDGMNELAIATAYILQGVKLALDYIHHMGYVHRSVKASHILISVDGKVVLSGLRSNLSMI 221
          HFMDGMNELAIATAYILQGVKLALDYIHHMGYVHRSVKASHILISDGKVVLSGLRSNLSMI
Sbjct 125 HFMDGMNELAIATAYILQGVKLALDYIHHMGYVHRSVKASHILISDGKVVLSGLRSNLSMI 184

Query 222 SHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVFFKD 281
          SHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVFFKD
Sbjct 185 SHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVFFKD 244

Query 282 MPATQMLLEKLNQTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPS 341
          MPATQMLLEKLNQTVPCLLDTSTIPAEELTMS SRS ANSGLSDSL TSTPR SNGDSPS
Sbjct 245 MPATQMLLEKLNQTVPCLLDTSTIPAEELTMSSTRSANSGLSDSLATSTPRPSNGDSPS 304

Query 342 HPYHRTFSPHFFHFVEQCLQRNPD RPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT 401
          HPYHRTFSPHFFHFVEQCLQRNPD RPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT
Sbjct 305 HPYHRTFSPHFFHFVEQCLQRNPDVRPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT 364

Query 402 NFEGSQSQDHSIGIFGLVTNLEELEVDWDEF 431
          NFEGSQ QDHSIGIFGLVTNLEELEVDWDEF

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Sbjct 365 NFEQSQDHSIGIFGLVTINLEELEVDDEWF 394

>ref|NP\_001015603.1| **UGM** STE20-related kinase adapter protein alpha [Bos taurus]  
 ref|NP\_001155356.1| **UG** STE20-related kinase adapter protein alpha [Ovis aries]  
 sp|Q5E9J9.1|STRAA\_BOVIN **G** RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD  
 alpha; AltName: Full=STE20-related adapter protein  
 gb|AA008938.1| **G** protein kinase LYK5 isoform 4 [Bos taurus]  
 gb|ACR46653.1| **G** STRADA [Ovis aries]  
 gb|DAA18360.1| **G** STE20-related kinase adapter protein alpha [Bos taurus]  
 Length=373

GENE ID: 515024 STRADA | STE20-related kinase adaptor alpha [Bos taurus]  
 (10 or fewer PubMed links)

Score = 748 bits (1932), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 356/373 (96%), Positives = 362/373 (98%), Gaps = 0/373 (0%)

Query	59	MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLQGE	118
		MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLQGE	
Sbjct	1	MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLQGE	60
Query	119	LHVSCLFNHPNIVPYRATFIADNELWVVTSMAYGSAKDLICTHFMDGMNELAIAYILQG	178
		LHVSCLF+HPNI+PY ATFIADNELWVVTSMAYGSAKDLICTHFMDGM+ELAIAYILQG	
Sbjct	61	LHVSCLFSPHNILPYGATFIADNELWVVTSMAYGSAKDLICTHFMDGMSLAIAYILQG	120
Query	179	VLKALDYIHMGYVHRSVKASHILISVDGKVVLSGLRSNLSMISHGQRQVRVHDFPKYSV	238
		LKALDYIHMGYVHRSVKASH+LIS DGKVVLSGLRSNLSMISHGQRQVRVHDFPKYS+	
Sbjct	121	ALKALDYIHMGYVHRSVKASHVLISADGKVVLSGLRSNLSMISHGQRQVRVHDFPKYSI	180
Query	239	KVLPWLSPEVLQQLQGYDAKSDIYSGITACELANGHVFPKDMPATQMLEKLNQTVPC	298
		KVLPWLSPEVLQQLQGYDAKSDIYSGITACELANGHVFPKDMPATQMLEKLNQTVPC	
Sbjct	181	KVLPWLSPEVLQQLQGYDAKSDIYSGITACELANGHVFPKDMPATQMLEKLNQTVPC	240
Query	299	LLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHPHYRTFSPHFHFVEQ	358
		LLDTSTIPAEELTMS SRS ANGLS+SL STPR SNGDSPSHPHYRTFSPHFHFVEQ	
Sbjct	241	LLDTSTIPAEELTMSRSANGLS+SLSTPRSTPRPSNGDSPSHPHYRTFSPHFHFVEQ	300
Query	359	CLQRNPDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPITTFEGSQSDHSGIFGLV	418
		CLQRNPD RPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT FEG SQSDHSGIFGLV	
Sbjct	301	CLQRNPDMPASASTLLNHSFFKQIKRRASEALPELLRPVTPITTFEGSQSDHSGIFGLV	360
Query	419	TNLEELEVDDEWF 431	
		TNLEELEVDDEWF	
Sbjct	361	TNLEELEVDDEWF 373	

>ref|NP\_082402.1| **UGM** STE20-related kinase adapter protein alpha [Mus musculus]  
 dbj|BAB27626.1| **G** unnamed protein product [Mus musculus]  
 gb|AAQ24157.1| **G** protein kinase LYK5 splice variant 1 [Mus musculus]  
 gb|AAH58517.1| **G** RIKEN cDNA 2610019A05 gene [Mus musculus]  
 gb|ABK42491.1| **G** STLK5 [synthetic construct]  
 emb|CAM27017.1| **G** novel protein [Mus musculus]  
 gb|EDL34272.1| **G** RIKEN cDNA 2610019A05, isoform CRA\_b [Mus musculus]  
 gb|EDL34273.1| **G** RIKEN cDNA 2610019A05, isoform CRA\_b [Mus musculus]  
 Length=394

GENE ID: 72149 Strada | STE20-related kinase adaptor alpha [Mus musculus]  
 (Over 10 PubMed links)

Score = 775 bits (2001), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 369/390 (95%), Positives = 380/390 (98%), Gaps = 0/390 (0%)

Query	42	TNDASSEIASFSKQEVMSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRR	101
		N+ASSEIASFSK E+MSSFLPEGGCYELLT+IGKGFEDLMTVNLARYKPTGEYVTVRR	
Sbjct	5	ANEASSEIASFSKPEMMSFLPEGGCYELLT+IGKGFEDLMTVNLARYKPTGEYVTVRR	64
Query	102	INLEACSNEMVTFLQGLHVSCLFNHPNIVPYRATFIADNELWVVTSMAYGSAKDLICT	161
		INLEACSNEMVTFLQGLHVSCLF+HPNIVPYRATFIADNELWVVTSMAYGSAKDLI T	
Sbjct	65	INLEACSNEMVTFLQGLHVSCLFSPHNIVPYRATFIADNELWVVTSMAYGSAKDLIGT	124
Query	162	HFMDGMNELAIAYILQGVKALDYIHMGYVHRSVKASHILISVDGKVVLSGLRSNLSMI	221
		HFMDGMNELAIAYILQGVKALDYIHMGYVHRSVKASHILIS DGKVVLSGLRSNLSMI	
Sbjct	125	HFMDGMNELAIAYILQGVKALDYIHMGYVHRSVKASHILISTDGKVVLSGLRSNLSMI	184
Query	222	SHGQRQVRVHDFPKYSVKVLPWLSPEVLQQLQGYDAKSDIYSGITACELANGHVFPKD	281
		SHGQRQVR VHDFFPKYS+KVLPWLSPEVLQQLQGYDAKSDIYSGITACELANGHVFPKD	
Sbjct	185	SHGQRQRAVHDFPKYSIKVLPWLSPEVLQQLQGYDAKSDIYSGITACELANGHVFPKD	244
Query	282	MPATQMLEKLNQTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPS	341
		MPATQMLEKLNQTVPCLLDTSTIPAEELTMSPSRS+AN GL+DSL +RPSNGDSPS	
Sbjct	245	MPATQMLEKLNQTVPCLLDTSTIPAEELTMSPSRSIANPGLNDSLAAAGSLRPSNGDSPS	304
Query	342	HPYHRTFSPHFHFVEQCLQRNPDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT	401
		HPYHRTFSPHFH+FVEQCLQRNPDARP+ASTLLNHSFFKQIKRRASEALPELLRPVTPIT	
Sbjct	305	HPYHRTFSPHFHFVEQCLQRNPDARPNASTLLNHSFFKQIKRRASEALPELLRPVTPIT	364
Query	402	NFEQSQSDHSGIFGLVTINLEELEVDDEWF 431	
		NFEQSQSDHSGIFGLVTINLE+LEVDDEWF	
Sbjct	365	NFEQSQSDHSGIFGLVTINLELDLEVDDEWF 394	

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>ref|NP_877972.1| UGM STE20-related kinase adapter protein alpha [Rattus norvegicus]
  sp|Q7TNZ6.1|STRAA RAT G RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD
  alpha; AltName: Full=STE20-related adapter protein
  gb|AAP92801.1| G protein kinase LYK5 [Rattus norvegicus]
  Length=393

  GENE ID: 303605 Strada | STE20-related kinase adaptor alpha [Rattus norvegicus]
  (10 or fewer PubMed links)

  Score = 758 bits (1958), Expect = 0.0, Method: Compositional matrix adjust.
  Identities = 362/390 (93%), Positives = 377/390 (97%), Gaps = 1/390 (0%)

  Query  42  TNDASSESIASFQKQEVMSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVIVRR  101
           N+ASSESIASFQK E+MSSFLPEGGCYELL+VIGKGFEDLMTVN +RYKPTGEYVIVRR
  Sbjct  5  ANEASSESIASFQKPEIMSSFLPEGGCYELLSVIGKGFEDLMTVN-SRYKPTGEYVIVRR  63

  Query  102  INLEACSNEMVTFIQGELHVSCLFNHPNIVPYRATFIADNELWVTSFPMAYGSAKDICT  161
           INLEACSNEMVTFIQGELHVSCLF+HPNIVPYRATFIADNELW VTSFPMAYGSAKDLI T
  Sbjct  64  INLEACSNEMVTFIQGELHVSCLFHPNIVPYRATFIADNELWAVTSFPMAYGSAKDICT  123

  Query  162  HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSNLSMI  221
           HFMDGM+ELAIAYILQGVLKALDYIHHMGYVHRSVKASHILIS DGVYLSGLRSNLSMI
  Sbjct  124  HFMDGMSNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISTDGVYLSGLRSNLSMI  183

  Query  222  SHGQRQRVVDHFPKYSVKVLPWLSPEVLQQLQGYDAKSDIYSVGITACELANGHVFFKD  281
           SHGQRQR VHDHFPKYS+KVLWLSPEVLQQLQGYDAKSDIYSVGITACELANGHVFFKD
  Sbjct  184  SHGQRQRAVDHFPKYSIKVLPWLSPEVLQQLQGYDAKSDIYSVGITACELANGHVFFKD  243

  Query  282  MPATQMLLEKINGTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPS  341
           MPATQMLLEKINGTVPCLLDTSTIPAEELTMSPSRS+AN GL+DSL +RP+NGDSPS
  Sbjct  244  MPATQMLLEKINGTVPCLLDTSTIPAEELTMSPSRSIANPGLNDSLAAAGSLRPANGDSPS  303

  Query  342  HPYHRTFSPPHFFHVEQCCLQRNPDPARPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT  401
           HPYHRTFSPPHFFHVEQCCLQRNPDPAR+ASTLLNHSFFKQIKRRASEALPELLRPVTPIT
  Sbjct  304  HPYHRTFSPPHFFHVEQCCLQRNPDPARNASTLLNHSFFKQIKRRASEALPELLRPVTPIT  363

  Query  402  NFEQSQSQDHSGLGLVTNLEELEVDWDEF  431
           +FEQSQSQDHSGL GLVTNLE+LEVDWDEF
  Sbjct  364  SFEQSQSQDHSGLGLVTNLEDEVDWDEF  393

```

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